

\$ dir \*.tan  
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*MOLV-RT vs Tag polymerase*

GAP of: Molvrtpro.Uw check: 5951 from: 1 to: 664

; molvrt.pro = Murine MoLV Rev. Transcriptase nts 2598-4589  
; Translated from file MOLV.SEQ on 20-Jun-90 at 01:03 PM  
; Edited on 20-Jun-90  
; File written by program SEQ on 20-Jun-90 at 01:33 PM

to: 6taqpolpro.Uw check: 7408 from: 1 to: 832

Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Nwsgappep.Cmp  
CompCheck: 1254

Gap Weight: 3.000 Average Match: 0.540  
Length Weight: 0.100 Average Mismatch: -0.396

Quality: 220.3 Length: 849  
Ratio: 0.332 Gaps: 29  
Percent Similarity: 43.277 Percent Identity: 20.247

Average quality based on 10 randomizations: 223.2 +/- 4.1

Molvrtpro.Uw x 6taqpolpro.Uw January 6, 1992 12:00 ..

```
1 .....TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGG 38
: : : : : : : : : : : : : : : : : : : : : : : :
1 MRGMLFLFEPKGRVLLVDGHHLAYRTFHALKGLTTSRGEPVQAVYGFAXS 50
39 MGLAVRQ..APLIIPKATSTPVSIIQYPMSEARLGIIKPHIQRLLDQGI 86
: : : : : : : : : : : : : : : : : : : : : : : :
51 LLKALKEDGDAVIVVFDKAPSRHEAYGGYKAGRAFTPEDFFROLALIK 100
87 LVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNRVED.....IHPTVP 130
: : : : : : : : : : : : : : : : : : : : : : : :
101 EL.....VDLLGLARLEVPGYEADDVLASLAKKAEKEGYEVRILTADK 143
131 NPYNLLSGLPFSHQWYTVLDLKDAPFC...LRLHPTSQPLFAFEWRDPEM 177
: : : : : : : : : : : : : : : : : : : : : : : :
144 DLYQLLS.....DRIHVLHPEGYLITPAWLWEKYGLRPGQWADYRALTG 187
178 GISGQLTWTRLPQGFKNSTPLFDE.....ALHRDLADFRIQHPDLILLQY 222
: : : : : : : : : : : : : : : : : : : : : : : :
188 DESDNLPQVK.GIGEKTARKLLEEWSLEALLKNLDRKPAIRKILAH. 235
223 VDDLILA.....ATSELDCCQGGTR.....ALLQTL 247
: : : : : : : : : : : : : : : : : : : : : : : :
236 MDDLKLSWDLAKVRTDLPLEVDFAKRREPDRERLRAFLEFGLSLLHEF 285
248 GNLGYRASAKKAQICQKQVKYLGILL..KEGQR..WLTEARKETVMGQPT 293
: : : : : : : : : : : : : : : : : : : : : : : :
286 GLLESPKALEEAPWPPPEGAFVGVLSRKEPMWADLLALAAARGGRVHRA 335
294 PKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGFDDQKA 343
: : : : : : : : : : : : : : : : : : : : : : : :
336 PEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLLDPSNT 385
344 YQEIK....QALLTAPALGLPDLTKPF.....ELFVDEKQGYAKGVLTQ 383
: : : : : : : : : : : : : : : : : : : : : : : :
386 TPEGVARRYGGEWTEEAGERAAALSERLFANLWGRLEGEERLLWLYREVER 435
```

```

436 FLSAVLAHMEATGVRLD.VAYLRALSLEVAEEIARLEAEVFRLA.GHPFN 483
433 .....VILAPHAVEALVK..QPPDRWLSNARMTHY.QALLDTRV 470
484 LNSRDQLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKIL 533
471 QFGPVVALNPATLLPLPE.....EGLQHNCLDILAEAHG....TRPDLT 511
534 QYRELTKLKSTYIDPLPDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQ 583
512 QPLPDA.....DHTWYTDGSSLL.....QEGQRKAGAAVTTETEVIWAKA 551
584 IPVRTPLGQRIRRAFIAGEGWLLVALDYSQIELRVLAHLSGDNLRVFO 633
552 LPAGTSAGRAELI.....ALTOALKMAE.....GKKLNVYTD 583
634 EGRDIHTETASWMFGVPREAVDPLMRRAKTINFGVLYGMSAHRLSQELA 683
584 SRYAFATAHIHG.....EIYRRRGL.....L 604
684 IPYEEAQAFIERYFQSFPKVRWIEKTLEEGRRRGYVETLFGRRRYVPDL 733
605 TSEGKEIKNKDEILAL.....LKALFLPKRLSIIHCPGH..... 638
734 EARVKSUREAAERMAFNMPVQGTADLMKLANVKLFPRLEEMGARMMLLOV 783
639 GKQHSAAEARGNRMADQAARKAAITET..... 664
784 HDELVLAPKERAEAVARLAKEVMGKVYPLAVPLEVEVGIGEDWLSAKE 832

```

\$ dir \*

MAIL>

molvrt.pro = Murine MoLV Rev. Transcriptase nts 2598-4589  
Sequence: MOLVRT.PRO Length: 664  
Listed from position 1 to position 664

```
1 TLNIEDEHRL HETSKEPDVS LGSTWLSDFP QAWAETGGMG LAVRQAPLII FLKATSTPVS
61 IKQYPMSEQA RLGKPHIQR LLDQGILVPC QSPWNTPLLP VKKPGTNDYR PVQDLREVNK
121 RVEDIHPTVP NPYNLLSGLP PSHQWYTVLD LKDAFFCLRL HPTSQPLFAF EWRDPFMGIS
181 GQLTWTRLPO GFKNSPTLFD EALHRDLADF RIQHPDLILL QYVDDLLLA TSELDCQOGT
241 RALLQTLGNL GYRASAKKAO ICQKQVKYLG YLLKEGQRWL TEARKETVMG QPTPKTPROL
301 REFLGTAGFC RLWIFGFAEM AAPLYPLTKT GTLFNWGPDQ QKAYQEIQA LLTAPALGLP
361 DLTKPFELFV DEKQGYAKGV LTQKLGPRR PVAYLSKKLD PVAAGWPPCL RMVAAIAVLT
421 KDAGKLTMGQ PLVILAPHAV EALVKQFPDR WLSNARMTHY QALLLDTDYR QFGPVVALNP
481 ATLLPLPEEG LQHNCLDILA EAHGTRPDLT DQFLPDADHT WYTDGSSLLQ EGQRKAGAAV
541 TTETEVIWAK ALPAGTSAQR AELIALTQAL KMAEGKKLVN YTDSDRYAFAT AHIHGEIYRR
601 RGLLTSEGKE IKNKDEILAL LKALFLPKRL SIIHCPGHOK GHSAEARGNR MADQAARKAA
661 ITET
```

#### Comments

Translated from file MOLV.SEQ on 20-Jun-90 at 01:03 PM  
Edited on 20-Jun-90  
File written by program SEQ on 20-Jun-90 at 01:33 PM

SEQ command: sta

#### ROUTINE TO CALCULATE SEQUENCE COMPOSITION

Do you want to use the whole sequence ? y

molvrt.pro = Murine MoLV Rev. Transcriptase nts 2598-4589  
Sequence: MOLVRT.PRO Length: 664 amino acids.  
Searched from position 1 to position 664  
Total # amino acids searched: 664

SEQ command:

ISOELECTRIC of: molvrtpro.uw Check: 5951 from: 1 to: 664 January 6, 1992 11:46

; molvrt.pro = Murine MoLV Rev. Transcriptase nts 2598-4589  
; Translated from file MOLV.SEQ on 20-Jun-90 at 01:03 PM  
; Edited on 20-Jun-90  
; File written by program SEQ on 20-Jun-90 at 01:33 PM

Amino Acid	Number of Residues
Arginine	36
Lysine	40
Histidine	18
Tyrosine	17
Cysteine	8
Glutamic Acid	35
Aspartic Acid	34

\$ TY TAQECO.RAN

GAP of: 6taqpolpro.Uw check: 7408 from: 1 to: 832

to: Ecopolapro.Uw check: 3547 from: 1 to: 928

DNA-directed DNA polymerase I (EC 2.7.7.7) - Escherichia coli

C:Species: Escherichia coli

C:Accession: A00718

R:Joyce, C.M., Kelley, W.S., and Grindley, N.D.F.

J. Biol. Chem. 257, 1958-1964, 1982 (Strain K12, sequence translated from the nucleotide sequence) . . .

Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Nwsgappep.Cmp  
CompCheck: 1254

Gap Weight: 3.000 Average Match: 0.540  
Length Weight: 0.100 Average Mismatch: -0.396

Quality: 609.1 Length: 938  
Ratio: 0.732 Gaps: 17  
Percent Similarity: 62.165 Percent Identity: 42.579

Average quality based on 10 randomizations: 277.0 +/- 5.7

6taqpolpro.Uw x Ecopolapro.Uw January 6, 1992 14:22 ..

```
1 MRGMLFLFEPKGRVLLVDGHHLAYRTFHALKGLTTSRGEFVQAVYG...F 47
  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
1 ...MVQI..PQNFLILVDGSSYLRYAHAFPLTNSAGEPTGAMYGVLMN 45
48 AKSLLKALKEDGDAVIVVFDKAPSFRHEAYGGYKAGRAPTFEDFFRQLA 97
  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
46 LRSLIMQYKPTHAA..VVFDKAGKTFRDELFEHYKSHRPFMPDDLRAQIE 93
98 LIKELVDLLGLARLEVFGYEADDVLASLAKKAEKEGYEVRILTADKDLYQ 147
  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
94 PLHAMVKAMGLPLLAVSGVEADDVIGTLAREAEKAGRPVLISTGDKDMAQ 143
148 LLSDRIHVLHP..EGYLITPAWLWEKYGLRFDQWADYRALTGDESDNLPQV 196
  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
144 LVTPNITLINTMTNTILGPEEVVNKYGVPPELIIDFLALMGDSSDNIPGV 193
197 KGIGEKTARKLLEEWGSLEALLKNLDRKLP.....AIREKILAHMDDL 239
  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
194 PGVGEKTAQALLQGLGGLDTLYAEPEKIAGLSFRGAKTMAAKLEQNKEVA 243
240 KLSWDLAKVRTDLPLEVDFAK..RREPDRERLRAFLERLEF..... 278
  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
244 YLSYQLATIKTDVELELTCEQLEVQQAEEELLGLFKKYEFKRWTADVEA 293
279 .....GSLLEHEFGLLLESP 291
  ::::: ::::: :::::
294 GKWLQAKGAKPAAKPQETSVADEAPEVTATVISYDNYVTILDEETLKAWI 343
292 KALEEAP.....WPPPEGAFVGFVLSRKEPMWADLLALA.....A 326
  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
344 AKLEKAPVFAFDTETDSLNDNISANLVGLSFA..IEPGVAAYIPVAHDYLD 392
327 ARGGRVHRAPEPYKAL.....RDLKEARGLLAK...DLSVLALRE 363
  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
393 PDQISRERALELLKPLLEDEKALKVGNLKYDRGILANYGIELRGIAFD 442
```

364 GLG.....LPPGDDPMLLAY...DPSNTTPEGVARRYGEW...  
 443 MLESYILNSVAGRHDMSLAERWLKHKITITFEEIAGKGKNQLTFTNQIALE 492  
 401 EAG....ERAALSERLFANLWGRLEGEERLLWLYREVERPLSAVLAHMEA 446  
 493 EAGRYAAEDADVTLQLHLKMWFDLQKHKGPLNVFENIEMPLVPVLSRIER 542  
 447 TGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLSRDLERVLFD 496  
 543 NGVKIDPKVLHNHSEELTLRLAELEKKAHEIAGEEFNLSSTKQLQTLFE 592  
 497 ELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTCLKSTYI 546  
 593 KQGIKPLKKT.PGGAPSTSEEVLEELALDYPLPKVILEYRGLAKLKSTYT 641  
 547 DPLPDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPTVPLGQRIRR 596  
 642 DKLPLMINPKTGRVHTSYHQAVTATGRLSSTDPNLQNIPTVRNEEGRRIRQ 691  
 597 AFIAEEGWLLVALDYSQIELRVLAHLSSDENLIRVFQEGRDIHTETASWM 646  
 692 AFIAPEDYVIVSADYSQIELRIMAHLSRDKGLLTAFAGKDIHRATAAEV 741  
 647 FGVPREAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPIYEEAQAFIERY 696  
 742 FGLPLETVTSEQRRSAKAINFGLIYGMSAFGLARQLNIPRKEAQKYMDLY 791

100% of the total population of the United States is now  
 living in the urban areas. The population of the United States  
 is now 100% of the total population of the United States.

100% of the total population of the United States is now

100% of the total population of the United States is now

\$ TY MOLVBSA.RAN

MOLVRT vs BSA

GAP of: Molvrtpro.Uw check: 5951 from: 1 to: 664

; molvrt.pro = Murine MolV Rev. Transcriptase nts 2598-4589  
; Translated from file MOLV.SEQ on 20-Jun-90 at 01:03 PM  
; Edited on 20-Jun-90  
; File written by program SEQ on 20-Jun-90 at 01:33 PM

to: Bsaprepro.Uw check: 7462 from: 1 to: 606

; Serum albumin precursor - Bovine  
; Alternate names: preproalbumin  
; Species: Bos primigenius taurus (cattle)  
; Accession: A03232  
; MacGillivray, R.T.A., Chung, D.W., and Davie, E.W. -- Eur. J. Biochem.  
; 98, 477-485, 1979 (Sequence of residues 1-32 with experimental details)  
.....

Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Nwsgappep.Cmp  
CompCheck: 1254

Gap Weight: 3.000 Average Match: 0.540  
Length Weight: 0.100 Average Mismatch: -0.396

Quality: 193.9 Length: 699  
Ratio: 0.320 Gaps: 17  
Percent Similarity: 40.806 Percent Identity: 17.513

Average quality based on 10 randomizations: 180.5 +/- 3.1

Molvrtpro.Uw x Bsaprepro.Uw January 6, 1992 14:08 ..

```
1 .....TLNIEDEHRLHETSKEPDVSLGSTW 25
1 MKWVTFISLLLLFSSAYSRGVFRDTHKSEIAHFKDLGEEHFKGLVLIA 50
26 LSDFFQAWAETGGMGLAVRQAPLIIPKATSTPVSIIQYPMSEARLGIIK 75
51 FSQYLQ.....QCPFDEHVKLVLNELTEFAKTCVADESHAGCE 87
76 PHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDI 125
88 KSLHTLFGDE.LCKVASLRETYGDMADCEKEQPERNECFLSHKDDSPDL 136
126 HPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP 175
137 PKLKPDPNTLCDEFKADKKF.....WGKYLVEIARRHP 170
176 EMGISGQLTWTRLPGGFKNSPTLFDEALHRDLADFRIGHPLILLQYVDD 225
171 YFYAPELLYANKYNGVFQEC.....QAEDKGACLLPKIET 206
226 LLLAATSELDCCQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGILLKE 275
207 MREKVLTSARQRLRCASIQKFGERALKAWS.VARLSQKFPKAEFVEVTK 255
276 GQRWLTEARKETVMGQPTPKTPRQLREFLGTCRLWIPGFAEMAAPLY 325
256 LVTDLTKVHKECCHGD.....LLECADDRADLAK.YICBBZBTISSKL 297
326 PLTKTGTLFNWGPDDQKAYQEIQALLTAPALGLPDLTKPFELFVDEKQG 375
298 KECKDPCLLEKSHCTAEVEKDAIPEDLPPLTADFAEDKDVCKNYQEAQDA 347
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1 .....TLNIEDEHRLHETSKEPDV.....SLGSTWLSDFQAWAETGG 38
      .|. : :| |.. : : :| : | : :| : :
1 TMITDSLAVVLQRRDWENPGVTQLNRLAAHPPFASWRNSE..EARTDRPS 48
      .
39 MGLAVRQAPLI IPLKATSTPV..SIKQYPMSEQEARLGKPHIQ..RLLDQG 85
      .| : : : : : : :| | : : : : : : :| : |..
49 QQLRSLNGEWRFAWFFAPEAVFESWLECDLPEADTVVVFPSNWQMHGYDAF 98
      .
86 IL..VPCQSPWNTPLLPVKKPGT.....NDYRF 111
      |. | : . | : :| : |.. : : ..
99 IYTNVTYPITVNPPFVPTENPTGCYSLTFNVDESWLQEGQTRIIFDGVNS 148
      .
112 VQDLREVNKRVE..DIHPTVPNPYNLLSGLPFSHOWYTVLDLK..... 152
      .| : : : : : : :| : : : :| | : : : :| : |
149 AFHLWCNGRWVGYGQDSRLPSEFDLSAFLRAGENRLAVMVLRWSDGSSYLE 198
      .
153 .....DAFFCLRLHFTSQPLFAFEWRD.....PEMGISG 181
      : : : : :| : :| : : : :|
199 DQDMWRMSGIFRDVSLHLHKPTTQISDFHVATRFNDDFSRAVLEAEVQMCQ 248
      .
182 QL.TWTRLPGGFKNSPTLFDEA...LHRDLADFRIQHPDLILLQYVDDL 227
      :| : :| : : : :| : : : :| :| : :| :| :| :| :| :| :|
249 ELRDYLRTVTVSLWQGETQVAGGTAPFGGEIIDERGGYADRVTLRL..NVE 296
      .
228 LAATSELDCCQGGTRALLQTLGNLGYRASAKKAQICQKQVKYL..GYLLKEG 276
      : .. : : :| : : : ..| |. : : : :| :| :| :|
297 NPKLWSAEIFNLVRAVVELHTADGTLIEAEACDVGFREVRIENGLLLLLNG 346
      .
277 QRWLTEA...RKETVMGQP.TPKTPRQLREFLGTAGFCRLWIPGFAEMA 321
      : : : : : : :| : :| : :| : :| : :| : :| : :|
347 KPLI IEGVNSPEHHPH LGGVMDQETMUDTIL MKQNNIENAVRCSHYEN 386

```

```

326 PLTKTGTLEFNWGPDDQKAYQEIQALLTAPALGLPDLTKPFELFVDERQG 375
. . . . . : : : : : . . . . . : : : : : . . . . . : : : :
298 KECKDPCLLEKSHCIAEVEKDAIPEDLPPLTADFAEDKDVCKNYQEAKDA 347
. . . . . : : : : : . . . . . : : : : : . . . . . : : : :
376 YAKGVLTKLGPWRRFPVAYLSKKLDFVAAGWFFCLRMVAAIAVLTKDAGK 425
. . . . . : : : : : . . . . . : : : : : . . . . . : : : :
348 FLGSFL...YEYSRRHPEYAVSVLLRLAKEYEATLEECCA.....KDDPH 389
. . . . . : : : : : . . . . . : : : : : . . . . . : : : :
426 LTMGQPLVILAPHAVEA..LVKQPPDRWLSNARMTHYQALLLDTDRVQFG 473
. . . . . : : : : : . . . . . : : : : : . . . . . : : : :
390 ACYTSVFDKLLKHLVDEPQNLIKQNCDDQFEKLGEGFQNALIVRYTR.... 435
. . . . . : : : : : . . . . . : : : : : . . . . . : : : :
474 PVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYT 523
. . . . . : : : : : . . . . . : : : : : . . . . . : : : :
436 KVPQVSTPTLVEVS.....RSLGKVGTRCCTKPESERMPCTEDYLSLIL 479
. . . . . : : : : : . . . . . : : : : : . . . . . : : : :
524 DGSSLLQEGQRKAGAAVTTETETEWAKALPAGTSAQRAELIALTQALKMA 573
. . . . . : : : : : . . . . . : : : : : . . . . . : : : :
480 NRLCVLHE.....KTFVESKVTKCCTESLVNRRFCFSALTP.....D 516
. . . . . : : : : : . . . . . : : : : : . . . . . : : : :
574 EGKKLNVYTDSRYAFATAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKA 623
. . . . . : : : : : . . . . . : : : : : . . . . . : : : :
517 ETYVPKAFDEKLFTF.....HADIC....TLPDTEKQIKKQATLVELLKH 557
. . . . . : : : : : . . . . . : : : : : . . . . . : : : :
624 LFLPKRLSIHCPGH.....QKGHSAEARGNRMADQAARKAAITET... 664
. . . . . : : : : : . . . . . : : : : : . . . . . : : : :
558 KPKATEEGLKTVMENFVAFVDKCCAADDKEACFAVEGPKLVVSTQTALA 606

```

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Aligning .....

Gaps: 29  
 Quality: 217.5  
 Quality Ratio: 0.328  
 % Similarity: 44.055  
 Length: 1031

Randomized alignment	Quality
1	223.5
2	210.2
3	216.4
4	211.1
5	208.6
6	214.9
7	216.8
8	212.9
9	211.5
10	213.2

Average quality based on 10 randomizations: 213.9 +/- 4.3



277 QRWLTEA....RKETV...TPKTPRQLREFLGTAGFCRLWIPG...EMA 321  
 347 KPLLIRGVNRHEHHPLHGQVMDEQTMVQDILLMKQNNFNNAVRC SHYPN:H 395  
 322 APLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVD 371  
 396 PLWYTLCDRYGLYVVDEANIETHGMVPMNRLTDDPRWLPAMSERVTRMVQ 445  
 372 EKQGYAKGVLTQKLGFWRRFPVAY...LSKKLDPVAAGWPPCLRMVA.... 414  
 446 RDRNHP.SVIIWSLGNESGHGANHDALYRWIKSVDFSRPVQYEGGGADTT 494  
 415 AIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWL..... 452  
 495 ATDIICPMYARVDEDOFPFAVPKWSIKKWLSLPGETRPLILCEYAHAMGN 544  
 453 SNARMTHYQALLLDTDRVQFGPVVALNPFATLLPLPEEGL..... 491  
 545 SLGGFAKYWQAFRQYFRLQGGFVWDVWQSLIKYDENGPNWSAYGGDFGD 594  
 492 ....QHNCLDILAEAHGT.RPDLTDQPLPD...ADHTW 521  
 595 TPNDROFCMNGLVFADRTPHFALTEAKHQQFFQFRLSGQTIEVTSEYLF 644  
 522 YTDGSSLLQ.....EGQRKAGAAVTTE.....TEVIWAKALFAGTSAQR. 560  
 645 RHSDNELLHWMVALDGKPLASGEVPLDVAPQKGQQLIELPELFQFESAGQL 694  
 561 .....AELIALTQALKMAEGKKLNVYTDSR..... 585  
 695 WLTVRVVQPNATAWSEAGHISAWQQWRLAENLSVTLPAASHAIPHLTTSE 744  
 586 ..YAFATAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSII 633  
 745 MDFCIELGNKRWQFNROSGFLS..QMWIGDKKQLLTPLRDQFTRAPLDND 792  
 634 HCPGHQKGHSAEARGNR..MADQAARKAAITET..... 664  
 793 IGVSEATRDPNAWVERWKAAGHYQAEAAALLQCTADTLADAVLITTAHAW 842

GAP of: Molvrtpro.Uw check: 9951 from: 1 to: 664

to: Phosbpro.Uw check: 1008 from: 1 to: 843

= phosphorylne B  
it)  $\sim \underline{97\text{KD}}$ .

```

; Glycogen phosphorylase (EC 2.4.1.1) - Rabbit
; Species: Oryctolagus cuniculus (domestic rabbit)
; Accession: A24302
; Nakano, K., Hwang, P.K., and Fletterick, R.J. -- FEBS Lett. 204, 283-287,
; 1986 (Sequence translated from the mRNA sequence)
; Title: Complete cDNA sequence for rabbit muscle glycogen phosphorylase.

```

Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Nwsgappep.Cmp  
CompCheck: 1254

Gap Weight: 3.0000      Average Match: 0.540  
Length Weight: 0.100      Average Mismatch: -0.396

Quality: 209.7 Length: 871  
Ratio: 0.316 Gaps: 24  
Percent Similarity: 43.396 Percent Identity: 16.667

Average quality based on 10 randomizations: 210.8 +/- 5.9

Molvrtpro.Uw x Phosbpro.Uw January 6, 1992 14:17 ..

```

1 .....TLNIE 5
51 DYYFALAHTVRDHLVGRWIRTQQHYEYKDPKRIYYLSLEFYMGRTLQNTM 100
6 DEHRLHETSKEP...DVSLGSTWLSDFPQAWAETGGMGLAVRQAFLLIIFLK 53
: 1.:.:1: :.:1: 1.:.:1: 1.:.:1:
101 VNLALENACDEATYQLGLDMEELEEIEED.AGLGNGGLGRLAACFLDSM. 148
54 ATSTPVSIIKQYPMSEQEARLGI...KPHIQRLLDQ.GILVPCQSPWNTPLL 99
: :.:1: :.:1: :.:1: :.:1: :.:1:
149 ...ATLGLAAYGYGIRYEFYGIFNQKICGGWQMEEADDWLRYGNPWEKARP 195
100 PVKKPGTNDYRPFVQDLREVNKRVE.....DIHPTVPNPFYNL 135
: :.:1: :.:1: :.:1: :.:1: :.:1:
196 EFTLP.VHFYGRVEHTSQGAKWVDTQVVLAMPYDTPVPGYRNNVNTMRL 244
136 LSGLPSSHQWYTVLDLKDFAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTW 185
: :.:1: :.:1: :.:1: :.:1: :.:1:
245 WSAKAPNDFNLKDFNVGGYIQAVLDRNLAENISRVLYPNDFNFEGKEL.. 292
186 TRLPQGFKNSPTLFDEALHR.DLADFRIQHPDLILLQYVDDLLLAATSEL 234
: :.:1: :.:1: :.:1: :.:1: :.:1:
293 .RLKQEYFVVAATLQDIIRRFKSSKFGCRDPVRTNFDAPDKVAIQLNDT 341
235 DCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLG.YLLKEGQRWLTEA 283
: :.:1: :.:1: :.:1: :.:1: :.:1:
342 HPSLAIPELMRVLVDLERLDWDKAWEVTVKTCAYTNHTVLPEALERWPH 391

```

284 RKETVMGQPTPKTPRQLREF.....TAGFCRLW..... 313  
 392 LLETLLPRHLQIIYEINQRFLNRVAAAFPGDVDRRLRRMSLVEEGAVKRIN 441  
 314 .....IPGFAEMAAPLYPLTKGTGLFNWGPD..QQKAYQEIQA 350  
 442 MAHLCIAGSHAVNGVARIHSEILKKTIFKDFEYELPHKFQNKTNGITPRR 491  
 351 LLTAPALGLPDLT.....KPFELFVDEKQGYAKGVLTQKL 385  
 492 WLVLCNPGLAETIAERIGEEYISDLQRLKLLSYVDD.EAFIRDVAKVKQ 540  
 386 GPWRRFPVAYLS.....KKLDPVAAGWPPCLRMVAAIAV 418  
 541 ENKLEKFAAYLEREYKVHINPNSLFDVQVKRIHEYKRQLLNCLHVITLYNR 590  
 419 LTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTD 468  
 591 IKKEPNKFVVPRTVMIGG.....KAAPGYHMAKMIIKLITAI...GD 629  
 469 RVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTQPLFDAD 518  
 630 VVNHDPPVVGDRRLRVI.....FLENYRVSLAEKVIPAADLSEQISTAGT 672  
 519 HTWYTDGSSLLQEGQRKAGAAVTTETE.....IWAKALPAGTSA 558  
 673 EASGTGNMKFMLNGALTIGTMDGANVEMAEAGEENFFIFGMRVEDVDRL 722  
 559 QRAELIALTQALKMAEGKK.LNVYTDSRYAFATAHIHGEI.....YRRR 601  
 723 DQRGYNAQEYYDRIPELRQIIIEQLSSGFFSPKQPDLFKDIVNMLMHDRF 772  
 602 GLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAE.....A 646  
 773 KVFADYEEYVKQDERVSALYKNPREWTRMVIRNIATSGKFSSDRTIAQYA 822  
 647 RGNRMADQAARKAAITET... 664  
 823 REIWGVEPSRQRLPAPDEKIP 843

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Aligning .....  
 ..

Gaps: 17  
 Quality: 609.1  
 Quality Ratio: 0.732  
 % Similarity: 62.165  
 Length: 938

Randomized alignment	Quality
1	283.2
2	272.2
3	277.9
4	275.8
5	280.7
6	279.1
7	282.7
8	268.3